

OY 301 GCCCACCACCTCTCTGATCTGTGAGAACAGTACCTGTGACTTCCCTTAAAGA 360
 Db 1867 GCCCACCACCTCTCTGATCTGTGAGAACAGTACCTGTGACTTCCCTTAAAGA 1926
 OY 361 CAATGTTGTGTAATCTTTGAAGACACACCGAAGACCTTATATCTGTGATCTTTACCC 420
 Db 1927 CAATGTTGTGTAATCTTTGAAGACACACCGAAGACCTTATATCTGTGATCTTTACCC 1986
 OY 421 CTTTCACTCTGCTTCTTCTTATGCTGCTATTCATTTAGTGAAGTGAAGAAAAAGATGACT 480
 Db 1987 CTTTCACTCTGCTTCTTCTTATGCTGCTT---CATGAATGATGAGAAAAAGATGACT 2043
 OY 481 CAGTTACAAAACACACCCAGACAA 508
 Db 2044 CAGTTAGGACACCAAAAAA 2071

RESULT 4

ACC50220 standard; cDNA; 2412 BP.

ACC50220;

12-JUN-2003 (first entry)

Breast cancer associated cDNA sequence SEQ ID NO:283.

Human; breast cancer; cytostatic; gene therapy; gene; ss.

Homo sapiens.

MO2003004989-A2.

16-JAN-2003.

21-JUN-2002; 2002WO-US19669.

21-JUN-2001; 2001US-299887P.

27-JUN-2001; 2001US-301572P.

18-JUL-2001; 2001US-306501P.

25-SEP-2001; 2001US-325002P.

05-MAR-2001; 2002US-362385P.

14-MAY-2002; 2002US-380391P.

(MILL-) MILLENIUM PHARM INC.

Lillie J, Gannavarrapu M, Glatt K, Hoersht S, Kamatkar S, Mertens M;

Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE, Bast RC;

Hortobagyi GN, Pusztai L, Meric F, Sahlin A, Mills GB;

WPI: 2003-210381/20.

P-PSDB; ABR47524.

Claim 1, SEQ ID 283; 128bp; English.

The present invention describes a method for assessing whether a patient

is afflicted with breast cancer. The method comprises comparing the level

of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and

ABR47386 to ABR47632) in a patient sample and the normal level of

expression of the marker in a control non-breast cancer sample, where a

significant increase in the level of expression of the marker in the

patient sample and the normal level is an indication that the patient is

afflicted with breast cancer. The breast cancer associated sequences

from the present invention have cytostatic activities and can be used in

gene therapy. The method is useful for diagnosing and treating breast

XX Sequence 2412 BP; 600 A; 696 C; 680 G; 436 T; 0 other;
 SQ

Query Match 62.5%; Score 424; DB 25; Length 2412;

Best Local Similarity 93.7%; Pred. No. 2,4e-126;

Matches 476; Conservative 0; Mismatches 25; Indels 7; Gaps 3;

OY 1 CTCGCTGACAGAGAAACCCCAACGCGAGAGAAAGAAATGGCCACACCTTGGGAA 60

Db 1903 CTCGCTGACAGAGAAACCCCAACGCGAGAGAAAGAAATGGCCACACCTTGGGAA 1962

OY 61 ACCTGTGTGGCCACACAGTCTTACGGGACAGAGACAGAGACAGAGACAGCCCTGACA 120

Db 1963 ACCTGTGTGGCCACACAGTCTTACGGGACAGAGACAGAGACAGAGACAGCCCTGACA 2019

OY 121 ACTGTTTCCCTCCACACAGCAGCATCTCTCCCTATTGGCTGTGCTTCCACTATA 180

Db 2020 ACTGTTTCCCTCCACACAGCAGCATCTCTCCCTATTGGCTGTGCTTCCACTATA 2078

OY 181 CACAGTCACCGTCCCAATGAGAAACAAGAGAGACACCCCTCCACATGAGACTCCACCTGC 240

Db 2079 CACAGTCACCGTCCCAATGAGAAACAAGAGAGACACCCCTCCACATGAGACTCCACCTGC 2138

OY 241 AAGTGAACAGCAGCATTCAGTCTGCACTGCTCCCTGCTTACTGATGACTCTGGCT 300

Db 2139 AAGTGAACAGCAGCATTCAGTCTGCACTGCTCCCTGCTTACTGATGACTCTGGCT 2198

OY 301 GCCCACCACCTCTCTGATCTGTGAGAACAGTACCTGTGACTTCCCTTAAAGA 360

Db 2199 GCCCACCACCTCTCTGATCTGTGAGAACAGTACCTGTGACTTCCCTTAAAGA 2258

OY 361 CAATGTTGTGTAATCTTTGAAGACACACCGAAGACCTTATATCTGTGATCTTTACCC 420

Db 2259 CAATGTTGTGTAATCTTTGAAGACACACCGAAGACCTTATATCTGTGATCTTTACCC 2318

OY 421 CTTTCACTCTGCTTCTTCTTATGCTGCTATTCATTTAGTGAAGTGAAGAAAAAGATGACT 480

Db 2319 CTTTCACTCTGCTTCTTCTTATGCTGCTT---CATGAATGATGAGAAAAAGATGACT 2375

OY 481 CAGTTACAAAACACCCAGACAA 508

Db 2376 CAGTTAGGACACCAAAAAA 2403

RESULT 5

ABR13359

ID ABR13359 standard; DNA; 3009 BP.

ABR13359;

30-JAN-2003 (first entry)

Breast specific related polynucleotide SEQ ID NO 74.

Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer;

metastatic; breast cancer; breast specific; human; ds.

Homo sapiens.

WO200277232-A2.

03-OCT-2002.

21-NOV-2001; 2001WO-US43815.

22-NOV-2000; 2000US-252509P.

(DIAD-) DIADEXUS INC.

Salceda S, Machina RA, Recipon H, Pluta J, Sun Y, Liu C;

WPI: 2003-018927/01.

| | | | |
|----|------|---|------|
| OY | 81 | CysLeuGIuGysGIyLeuPheThrCysLysSerGysGIyAValAlHisProGIuGIu | 100 |
| Db | 415 | TGcCTGGAATGGcCTTtACCTtCGCAAAAGcTgtGGcCGcGTtCACCCGAGAGAG | 474 |
| OY | 101 | GIyTrpIleCysAspProCysHisLeuAlaArgValAllysIleGIySerLeuGIutrp | 120 |
| Db | 475 | GGcTGGATtGTtGACCCtGTtCACTtGGCCAGAGtCGtGAAGAtCGGtCACTAGtGG | 534 |
| OY | 121 | TyrTrpGIuHisValLysAlaArgPheLysArgPheGIySerAlaLysValIleArgSer | 140 |
| Db | 535 | TACtATGAGcATGTGAAGAGCCCGcTTCAGAGGTTCGAAAGtGCCAAGGTATCGGGTtCC | 594 |
| OY | 141 | LeuHisGIyAArgLeuAGInGIyAlaGIyProGIuLeuIleSerGIuGIuArgSerGIy | 160 |
| Db | 595 | CTtCACAGGGcCGcGTtCGAGGGtGGAGcGTtGGcCTtACCTGATtGTtGAAGAGAGtGGA | 654 |
| OY | 161 | AspSerAspGIuThrAspGIuAspGIyGIuProGIySerGIuAlaGIuAlaGIu | 180 |
| Db | 655 | GACAGCGACCGACAGATGAGAGAtGGAGAACTGGtCTtCAGAGGGCCAGGCCAGGCCAG | 714 |
| OY | 181 | ProPheGIySerLysLysArgLeuSerValHisAspPheAspPheGIuGIyAsp | 200 |
| Db | 715 | CCCTtTGGACACAA----- | 729 |
| OY | 201 | SerAspAspSerThrGIuProGIuGIyHisSerLeuHisLeuSerSerValProGIuAla | 220 |
| Db | 729 | ----- | 729 |
| OY | 221 | ArgAspSerProGIuSerLeuThrAspGIuSerCysSerGIuLysAlaAlaProHisLys | 240 |
| Db | 730 | -----TCCtCACAGAtGAGtCTtGTtCAGAGAGAGCGCCtCACAG | 774 |
| OY | 241 | AlaGIuGIyLeuGIuGIuAlaAspThrGIyAlaSerGIyCysHisSerHisProGIuGIu | 260 |
| Db | 775 | GCTAGAGGGCCtGGAGAGCGcTGAACtGGGGCCtCTtGGGTtCCtCCACtCCGAGAG | 834 |
| OY | 261 | GIuProThrSerIleSerProSerArgHisGIyAlaLeuAlaGIuLeuCysProProGIy | 280 |
| Db | 835 | CAGCGACGACATCTtCACCTtCCAGACAGCGGGCCcGTtGAGtCTtGCCCGCGtTGA | 894 |
| OY | 281 | GlySerHisArgMetAlaLeuGIyThrAlaAlaAlaLeuGIySerAsnValIleArgAsn | 300 |
| Db | 895 | GGcTCCACAGAGAGtGGCCtGGGAGtCGtCTtGCACtCGGGtCGAAtGTtCATCAGAGAt | 954 |
| OY | 301 | GIuGIuLeuProLeuGIuIntYrLeuAlaAspValAspHisPheSerAspGIuGIuSerIleArg | 320 |
| Db | 955 | GAGAGcGTtCCCGcAGtACTtGTtGGCCAGtGTtGACACtCTtGATtGAGGAAGAtCCCG | 1014 |
| OY | 321 | AlaHisValMetAlaSerHisHisSerLysArgArgGIyAlaArgAlaSerSerGIuSerGIu | 340 |
| Db | 1015 | GCTACGTGAtGGcCTtCCACACAtTtCCAGCGGAGAGCGCGGGcCTtCTtCGAGAGtCAG | 1074 |
| OY | 341 | IlePheGIuLeuAsnLysArgIleSerAlaValaGIuCysLeuLeuThrTyrLeuGIuAsn | 360 |
| Db | 1074 | ----- | 1074 |
| OY | 361 | ThrValValProProLeuAlaLysGIyLeuGIyAlaGIyAlaArgThrGIuAlaAspVal | 380 |
| Db | 1075 | -----GGtCTAGtGTtCTtGAGAGCGCCAGCGAGCGCGAGtGA | 1110 |
| OY | 381 | GIuGIuGIuAlaLeuArgArgLysLeuGIuGIuLeuThrSerAsnValSerAspGIuGIu | 400 |
| Db | 1111 | GAGAGAGAGCGCCtCGAGAGAGAGtCGAGAGcGTtGACACAGtCAAGtGACACAGAG | 1170 |
| OY | 401 | ThrSerSerGIuGIuGIuAlaLysAspGIuLysAlaGIuProAsnArgAspLysSer | 420 |
| Db | 1171 | ACCTGtCTtCGAGAGAGtCCAAAGAGCAAAAGCAGAGCCCAAGGGAACAAtTCA | 1230 |
| OY | 421 | ValGIyProLeuProGIuAlaAspProGIuValaGIyThrAlaAlaHisGIuThrAsnArg | 440 |
| Db | 1231 | GTtTGGGGcCTtCCCGcAGCGAGtCCGAGAGtGGCGAGcGTtGCCATCAAAACCAACAGA | 1290 |

QY 441 GlnGluLysSerProGlnAspProGlnAspProValGlnTyrAsnAlaGlyThrAspGlu 460
Db 1291 CAGGAAAAAGCCCCCGAGACCTGGGGACCCCGTCAGTCAACAGACGACGATGAG 1350
QY 461 GluLeuSerGluLeuGlnAspArgValAlaValThrAlaSerGluValGlnGlnAlaGlu 480
Db 1351 GAGCTGCAGAGCTGGAGGACAGAGTGCAGTGCAGGCTTCAGAAAGTCCAGCAGCAGAG 1410
QY 481 SerGluValSerAspIleGluSerArgIleAlaAlaLeuArgAlaAlaGlyLeuThrVal 500
Db 1411 AGCAGAGTTTCAGACATGTAATCCAGATTCACCCCTGAGGCGCCGAGGCTCAGCGTG 1470
QY 501 LysProSerGluLysProArgArgLysSerAsnLeuProIlePheLeuProArgValAla 520
Db 1471 AAGCCTCGGGAAAGCCCCCGAGGAGTCAAACTCCGATATTTCCTCCGAGTGCT 1530
QY 521 GlyLysLeuGluLysArgProGlnAspProAsnAlaAspProSerSerGluAlaLysAla 540
Db 1531 GGGAAACTTGGCAGAGACAGACGAGCCCAATCCAGACCTTCAGTGAAGGCCAGGCA 1590
QY 541 MetaAlaValProTyrLeuLeuArgArgLysPheSerAsnSerLeuLysSerGlnGlyLys 560
Db 1591 ATGGCTGTGCCCTATCTTCAGAGAAAGTTCAGTATTCCTCGAAAGTCAAGTAA 1650
QY 561 AspAspAspSerPheAspArgLysSerValTyrArgLysLeuThrGlnAlaGlnPro 580
Db 1651 GATATGATCTTTTGTGATCGGAAATCAGTACCGAGGCTCGTGACACAGAGAAACCCC 1710
QY 581 AsnAlaArgLysGluMetAlaSerHisThrPheAlaLysProValValAlaHisGlnSer 600
Db 1711 AACCCGAGGAAGAGATGCCAGCCACACTTCGGAACCTGTGTGGCCACCAAGTCC 1770

RESULT 4
US-10-106-698-304
; Sequence 304, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106, 698
; PRIOR APPLICATION NUMBER: 2002-03-27
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 304
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-304

Alignment Scores:
Pred. No.: 1,07e-109 Length: 1257
Score: 1295.00 Matches: 271
Percent Similarity: 88.89% Conservative: 1
Best Local Similarity: 88.56% Mismatches: 6
Query Match: 41.81% Indels: 30
DB: 14 Gaps: 1

US-09-995-494-96 (1-600) x US-10-106-698-304 (1-1257)

QY 295 SerAsnValIleArgAsnGlnGlnLeuProLeuGlnTyrLeuAlaAspValAspThrSer 314
Db 1 TCGAATGTATCATGAGATGAGCAGCTGCCCTCAGTACTTGGCCATGTGACACCTCT 60
QY 315 AspGluGluSerIleArgAlaHisValMetAlaSerHisHisSerLysArgGlyArg 334
Db 61 GATGAGAAAGCATCCGGGCTCAGTGTAGTGCCTCCACCATTCGAAGGAGAGGCCGG 120

QY 335 AlaSerSerGluSerGlnIlePheGluLeuAsnLysArgIleSerAlaValGluLysLeu 354
Db 121 GCGTCTTCGAGACTCAG----- 138
QY 355 LeuThrTyrLeuGlnGluAsnThrValValProProLeuAlaLysGlyLeuGlyVal 374
Db 139 -----GCTTAAAGTGTCTGAKYK 156
QY 375 ArgThrGluAlaAspValGluGlnGluAlaLeuArgArgLysLeuGluGluLeuThrSer 394
Db 157 CGCACAGAGGCCCGATGTAGAGAGAGAGGCCCTGAGAGGAACTGGAGGAGCTGACACAGC 216
QY 395 AsnValSerAspGlnGluThrSerSerGluGlnGluGluAlaLysAspGluLysAlaGlu 414
Db 217 AACCTCAGTGCACGAGGAGCTGCTCCGAGAGGAGAGTCCAGAGCAGAAAGGACAGAG 276
QY 415 ProAsnArgAspLysSerValGlyProLeuProGlnAlaAspProGluValGlyThrAla 434
Db 277 CCNACAGAGGCAATCAGTTGGGCTCTCCCGAGGCGGACCCGAGAGT- GGCACGCT 335
QY 435 AlaHisGlnThrAsnArgGlnGluLysSerProGlnAspProGlnAspProValGlnTyr 454
Db 336 GCGCATCAAAACCAACAGACAGGAAAAAGCCCCAGAGACCTGGGGACCCCTCCAGTAC 395
QY 455 AsnArgThrThrAspGluGluLeuSerGluLeuGlnAspArgValAlaValThrAlaSer 474
Db 396 AACGAGCCACAGATGAGAGCTCTCAGAGCTGAGAGACAGTGGAGTACGCGCTCA 455
QY 475 GluValGlnGlnAlaGluSerGluValSerAspIleGluSerArgIleAlaLysLeuArg 494
Db 456 GAAGTCCAGCAGGAGAGAGCAGGCTTCAGACATTAAATCCAGATTKAGCCCTGAGC 515
QY 495 AlaAlaGlyLeuThrValLysProSerGlyLysProArgArgLysSerAsnLeuProIle 514
Db 516 GCCGAGGCTC-ACGCTGAAGCCCTCGGAAAGCCCGGAGGAGGAACTCAAACTCCGATA 574
QY 515 PheLeuProArgValAlaGlyLysLeuGlyLysArgProGlnAspProAsnAlaAspPro 534
Db 575 TTTCTCCCTGAGGCTGGGAAACTTGGCAAGGACCAAGGACCCCAATTCGACAGCCCT 634
QY 535 SerSerGluAlaLysAlaMetAlaValProTyrLeuLeuArgArgLysPheSerAsnSer 554
Db 635 TCAAGTAGGCGCAAGCAATGCTGCTCCCTATCTTGGAAAGAAAGTTCAGTATTC 694
QY 555 LeuLysSerGlnGlyLysAspAspAspSerPheAspArgLysSerValTyrArgGlySer 574
Db 695 CTGAAAAGTCAAGGTAAAGATGATTTCTTTGATCGAAATCAAGTACCGAGGCTCG 754
QY 575 LeuThrGlnArgAsnProAsnAlaArgLysGlyMetAlaSerHisThrPheAlaLysPro 594
Db 755 CTGACACAGAGAAACCCCAAGCGGAGGAAAGGATGCGCACACACTTCGGGAAACCT 814
QY 595 ValValAlaHisGlnSer 600
Db 815 GTGGTGGCCCAACCAAGTCC 832

RESULT 5
US-09-764-891-238
; Sequence 238, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764, 891
; PRIOR APPLICATION NUMBER: 2001-01-17
; PRIOR APPLICATION data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 762
; TYPE: DNA